

RESPONSE TO RESTRICTION REQUIREMENT
U.S. Appln. No. 10/535,414 (Q87920)

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

Claim 1. (Cancelled).

Claim 2. (Currently Amended) A set of oligonucleotide probes ~~as claimed in claim 1~~, wherein said set consists of not more than 1000 oligonucleotide probes and said set comprises each of the following 351 oligonucleotides ~~probes are each selected from:~~

~~an oligonucleotide: having at the~~ sequences as set forth in

SEQ ID Nos. 1, 2, 3, 4, 5, 11, 12, 13, 19, 25, 31, 32, 33, 34, 36, 37, 39, 45, 46, 47, 48, 50, 55, 56, 60, 61, 64, 66, 68, 73, 74, 75, 76, 77, 78, 80, 83, 85, 86, 90, 96, 98, 99, 100, 101, 105, 106, 107, 109, 111, 114, 115, 116, 117, 119, 120, 121, 122, 123, 124, 125, 127, 128, 130, 131, 132, 133, 135, 136, 137, 138, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 161, 162, 163, ~~164~~, 165, 166, 168, 169, 171, 173, 174, 175, 176, 177, 178, 179, 180, 182, 183, 185, 186, 187, 190, 191, 195, 197, 198, 199, 200, 202, 204, 206, 207, 210, 212, 214, 216, 217, 218, 219, 220, 221, 222, 224, 225, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 243, 244, 245, 249, 251, 256, 258, 259, 260, 261, 262, 267, 268, 270, 272, 273, 274, 275, 276, 278, 279, 280, 282, 284, 286, 287, 289, 291, 292, 295, 296, 297, 298, 299, 301, 303, 305, 307, 308, 309, 310, 311, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 361, 363, 364, 365, 366, 367, 368, 369, 370, 371, 374, 375,

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472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 484, 487,
489, 490, 496, 497, 498, 499 ~~or~~ and 501, ~~or~~

-with the proviso that any of said 351 oligonucleotides or a combination thereof may be replaced in said set with (i) an oligonucleotide fragment(s) of the respective said sequence oligonucleotide(s) being replaced, which fragment is at least 15 bases—nucleotides in length, (ii) ~~or~~ an oligonucleotide(s) with a complementary having a sequence complementary to the respective oligonucleotide(s) being replaced, or (iii) a functionally equivalent an oligonucleotide(s) which is functionally equivalent to the respective oligonucleotide(s) being replaced and which hybridizes under conditions of high stringency to any of said aforementioned the respective oligonucleotide(s) being replaced.

Claim 3. (Cancelled)

Claim 4. (Currently Amended) AThe set of oligonucleotide probes as claimed in claim ~~1~~2, wherein each probe in said set binds to a different transcript.

Claim 5. (Currently Amended) AThe set as claimed in claim ~~2~~1, wherein said set consists of ~~from 10 to~~ not more than 500 oligonucleotide probes.

Claims 6-8. (Cancelled).

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Claim 9. (Currently Amended) AThe set of oligonucleotide probes as claimed in claim 12, wherein said probes are immobilized on one or more solid supports.

Claims 10-12. (Cancelled).

Claim 13. (Currently Amended) A kit comprising a set of oligonucleotide probes as claimed in claim 21 immobilized on one or more solid supports.

Claims 14-15. (Cancelled).

Claim 16. (Currently Amended) A method for determining the gene expression pattern of a cell, comprising at least the steps of:

- a) isolating mRNA from said cell, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step a) to a set of oligonucleotide probes as defined in claim 12; and
- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern.

Claim 17. (Currently Amended) A method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

- a) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step a) to a set of oligonucleotide probes as defined in claim 12 specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

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- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotide probes bind, in the sample with the disease, condition or stage thereof.

Claim 18. (Currently Amended) A method of preparing a test gene transcript pattern comprising at least the steps of:

- a) isolating mRNA from the cells of a sample of said test organism, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step a) to a set of oligonucleotide probes as defined in claim 21 specific for a disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and
- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern, which reflects the level of gene expression of genes to which said oligonucleotide probes bind, in said sample.

Claim 19. (Currently Amended) A method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

- a) isolating mRNA from the cells of a sample of said organism, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step a) to a set of oligonucleotide probes as defined in claim 12

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- specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation;
- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotide probes bind in said sample; and
 - d) comparing said pattern to a standard diagnostic pattern prepared by
 - i) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;
 - ii) hybridizing the mRNA or cDNA of step i) to said set of oligonucleotides probes; and
 - iii) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in the sample with the disease, condition or stage thereof, wherein the sample is from an organism corresponding to the organism and sample under investigation,

to thereby determine the degree of correlation indicative of the presence of said disease or condition or a stage thereof in the organism under investigation.

Claims 20-22. (Cancelled).

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Claim 23. (Currently Amended) ~~A~~The method as claimed in claim 17, wherein ~~said probes are oligonucleotide probes selected from:~~

~~an oligonucleotide having a sequence as set forth in SEQ ID No.~~

~~1, 2, 3, 4, 5, 11, 12, 13, 19, 25, 31, 32, 33, 34, 36, 37, 39, 45, 46, 47, 48, 50, 55, 56, 60, 61, 64, 66, 68, 73, 74, 75, 76, 77, 78, 80, 83, 85, 86, 90, 96, 98, 99, 100, 101, 105, 106, 107, 109, 111, 114, 115, 116, 117, 119, 120, 121, 122, 123, 124, 125, 127, 128, 130, 131, 132, 133, 135, 136, 137, 138, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 161, 162, 163, 164, 165, 166, 168, 169, 171, 173, 174, 175, 176, 177, 178, 179, 180, 182, 183, 185, 186, 187, 190, 191, 195, 197, 198, 199, 200, 202, 204, 206, 207, 210, 212, 214, 216, 217, 218, 219, 220, 221, 222, 224, 225, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 243, 244, 245, 249, 251, 256, 258, 259, 260, 261, 262, 267, 268, 270, 272, 273, 274, 275, 276, 278, 279, 280, 282, 284, 286, 287, 289, 291, 292, 295, 296, 297, 298, 299, 301, 303, 305, 307, 308, 309, 310, 311, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 361, 363, 364, 365, 366, 367, 368, 369, 370, 371, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 457, 458, 459, 460, 461, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473,~~

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~~474, 475, 476, 477, 478, 479, 480, 481, 482, 484, 487, 489, 490,
496, 497, 498, 499 or 501,~~

~~or an oligonucleotide fragment of said sequence, which fragment
is at least 15 bases to length, or an oligonucleotide with a
complementary sequence, or a functionally equivalent
oligonucleotide which hybridizes under conditions of high
stringency to any of said aforementioned oligonucleotides and said
disease is breast cancer.~~

Claims 24-27. (Cancelled).

Claim 28. (Currently Amended) AThe method as claimed in
claim 17, wherein said pattern is expressed as an array of numbers
relating to the expression level associated with each probe.

Claim 29. (Currently Amended) AThe method as claimed in
claim 17, wherein said organism is a eukaryotic organism, preferably
a mammal.

Claim 30. (Currently Amended) AThe method as claimed in
claim 29 wherein said organism is a human.

Claim 31. (Cancelled).

Claim 32. (Currently Amended) AThe method as claimed in
claim 17, wherein said disease is cancer or a degenerative brain
disorder.

Claim 33. (Currently Amended) AThe method as claimed in
claim 17, wherein said sample is tissue, body fluid or body waste.

Claim 34. (Currently Amended) AThe method as claimed in
claim 17, wherein said sample is peripheral blood.

Claim 35. (Currently Amended) AThe method as claimed in
claim 17, wherein the cells in the sample are not disease cells, have
not been in contact with such cells and do not originate from the site
of the disease or condition.

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Claims 36-37. (Cancelled).